CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/722,544A

ENTERED

CRF Processing Date: 3/25/2002
Edited by: _____
Verified by: _____ AL (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

✓ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: 3 _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 03/25/2002
PATENT APPLICATION: US/09/722,544A   TIME: 12:43:36

Input Set : A:\07334-362001.txt
Output Set: N:\CRF3\03222002\I722544A.raw

p.6

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 3 <110> APPLICANT: Hong, Chen
 4         Freimer, Nelson B.
 6 <120> TITLE OF INVENTION: METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS
 8 <130> FILE REFERENCE: 07334-362001
10 <140> CURRENT APPLICATION NUMBER: 09/722,544A
11 <141> CURRENT FILING DATE: 2000-11-28
13 <150> PRIOR APPLICATION NUMBER: 09/236,134
14 <151> PRIOR FILING DATE: 1999-01-22
16 <150> PRIOR APPLICATION NUMBER: 60/078,044
17 <151> PRIOR FILING DATE: 1998-03-16
19 <150> PRIOR APPLICATION NUMBER: 60/088,312
20 <151> PRIOR FILING DATE: 1998-06-05
22 <150> PRIOR APPLICATION NUMBER: 60/106,056
23 <151> PRIOR FILING DATE: 1998-10-28
25 <160> NUMBER OF SEQ ID NOS: 33
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0
29 <210> SEQ ID NO: 1
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31 <212> TYPE: DNA
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41 gcatcttagg aatgacagag ttgcgtccct ctctgttgcc aggctggagt tcagtggcat     180
42 gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctccca cctcagcccc     240
43 atgaggacct gggactacag gacacagcta aatccctgac acgg atg aaa att aaa     296
44                                                   Met Lys Ile Lys
45                                                     1
47 gca gag aaa aac gaa ggt cct tcc aga agc tgg tgg caa ctt cac tgg     344
48 Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His Trp
49   5                   10                  15                  20
51 gga gat att gca aat aac agc ggg aac atg aag ccg cca ctc ttg gtg     392
52 Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val
53                   25                  30                  35
55 ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca ccc act     440
56 Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro Thr
57               40                  45                  50
59 tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt tct gag     488
60 Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu
61           55                  60                  65
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63 gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt      536
64 Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly
65      70                      75                  80
67 att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc      584
68 Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr
69 85                      90                  95              100
71 aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc      632
72 Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala
73                  105                 110                 115
75 ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg      680
76 Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg
77              120                 125                 130
79 cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc      728
80 Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys
81          135                 140                 145
83 ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct agc tgg      776
84 Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp
85      150                 155                 160
87 tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata tat caa      824
88 Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile Tyr Gln
89 165                 170                 175             180
91 ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc atc agt      872
92 Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro Ile Ser
93                  185                 190                 195
95 gaa aag ctc att gag gaa gat gca caa ttg acc caa atg gag gat gtg      920
96 Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu Asp Val
97              200                 205                 210
99 ttc agc cag ttg act gtg gat gtg aat tct ctc ttt aac agg agt ttt      968
100 Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg Ser Phe
101          215                 220                 225
103 aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt caa tca     1016
104 Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe Gln Ser
105      230                 235                 240
107 cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt cca gct     1064
108 His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe Pro Ala
109 245                 250                 255             260
111 ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt tgg gac     1112
112 Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys Trp Asp
113                  265                 270                 275
115 att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct att tat     1160
116 Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser Ile Tyr
117              280                 285                 290
119 gaa agt gtc agt gaa aca att act aag atg ctg aag gca ata gaa gat     1208
120 Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile Glu Asp
121          295                 300                 305
123 tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att tca aag     1256
124 Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile Ser Lys
125      310                 315                 320
127 atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac cag aat     1304
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128 Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp Gln Asn
129 325                 330                 335                 340
131 ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt cag gct   1352
132 Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys Gln Ala
133                 345                 350                 355
135 cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta   1400
136 His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu
137                 360                 365                 370
139 gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat ggc cag   1448
140 Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr Gly Gln
141             375                 380                 385
143 att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat ctg gtg   1496
144 Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr Leu Val
145         390                 395                 400
147 gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca aac cag   1544
148 Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala Asn Gln
149 405                 410                 415                 420
151 gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg   1592
152 Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg
153                 425                 430                 435
155 att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac   1640
156 Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp
157             440                 445                 450
159 tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct ctt gaa   1688
160 Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro Leu Glu
161         455                 460                 465
163 gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca aaa gct   1736
164 Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala Lys Ala
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167 cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc taatgcatcc   1789
168 Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
169 485                 490                 495
171 tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga aataaaaaag   1849
172 gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg aagtactctt   1909
173 agtttactta tgttgaatgg cttagctatt aatactcaaa ttgagttaaa atgaaaattc   1969
174 ctccttaaaa aatcaaacgt aatatgtatt acatttcatg gtacattagt agttctttgt   2029
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178 <211> LENGTH: 495
179 <212> TYPE: PRT
180 <213> ORGANISM: Homo sapiens
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186             20                  25                  30
187 Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His
188         35                  40                  45
189 Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys
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194                 85                    90                    95
195 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu
196                 100                   105                   110
197 Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu
198             115                   120                   125
199 Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu
200         130                   135                   140
201 Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys
202 145                   150                   155                   160
203 Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg
204                 165                   170                   175
205 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp
206                 180                   185                   190
207 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln
208             195                   200                   205
209 Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe
210     210                   215                   220
211 Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln
212 225                   230                   235                   240
213 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr
214                 245                   250                   255
215 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu
216             260                   265                   270
217 Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser
218         275                   280                   285
219 Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys
220     290                   295                   300
221 Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly
222 305                   310                   315                   320
223 Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu
224                 325                   330                   335
225 Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln
226             340                   345                   350
227 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu
228         355                   360                   365
229 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln
230     370                   375                   380
231 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr
232 385                   390                   395                   400
233 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu
234                 405                   410                   415
235 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln
236             420                   425                   430
237 Val Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr
238     435                   440                   445
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240     450                 455             460
241 Ile Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val
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258 gcatcttagg aatgacagag ttgcgtccct ctckgttgcc aggctggagt tcagtggcat  180
259 gttcwtagct cactgaagcc tcaaattcct gggttcaagt gaccctccya cctcagcccc  240
260 atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc     288
261 Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu
262   1               5                   10                  15
264 ttg gtg ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca     336
265 Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala
266             20                  25                  30
268 ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt     384
269 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
270             35                  40                  45
272 tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg     432
273 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu
274     50                  55                  60
276 act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa     480
277 Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu
278 65                  70                  75                  80
280 cac acc aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag     528
281 His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln
282             85                  90                  95
284 gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa     576
285 Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu
286             100                 105                 110
288 gaa agg cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg     624
289 Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg
290             115                 120                 125
292 tct tgc ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct     672
293 Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro
294     130                 135                 140
296 agc tgg tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata     720
297 Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile
298 145                 150                 155                 160
300 tat caa ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc     768
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/25/2002
PATENT APPLICATION: US/09/722,544A   TIME: 12:43:38

Input Set : A:\07334-362001.txt
Output Set: N:\CRF3\03222002\I722544A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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